Amendments to the Claims:

This listing of claims will replace all previous versions and listings of claims in the application:

1-24 (canceled)

25. (currently amended) A method for measuring the ~~gene~~ expression level of at least two target genes in a biological sample, comprising

(a) providing a polynucleotide complementary to an intronic RNA sequence within ~~a~~ said target genes ~~gene~~, wherein the expression of said intronic RNA sequence has been confirmed to correlate ~~correlates~~ with the expression of an exonic mRNA sequence within said target genes ~~gene~~;

(b) hybridizing said polynucleotide to said intronic RNA sequence to form a polynucleotide-intronic RNA complex; and

(c) detecting and identifying the polynucleotide-intronic RNA complex;

(d) determining the gene expression level of said target genes in the biological sample.

26. (original) The method of claim 25 wherein said intronic RNA sequence is selected by identifying intronic sequences which are co-expressed with the mRNA of said target gene, and selecting an intronic RNA sequence having the highest correlation coefficient for said co-expression.

27. (original) The method of claim 25 wherein said intronic RNA sequence is at least 50 nucleotide bases long.

28. (original) The method of claim 25 wherein said biological sample is a tissue sample.

29. (original) The method of claim 28 wherein said tissue is a tumor tissue.

30. (original) The method of claim 29 wherein said tumor is cancer.

31. (original) The method of claim 30 wherein said cancer is selected from the group consisting of breast cancer, colon cancer, lung cancer, prostate cancer, hepatocellular cancer, gastric cancer, pancreatic cancer, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, thyroid cancer, renal cancer, carcinoma, melanoma, and brain cancer.

32. (original) The method of claim 28 wherein said tissue sample is a fixed, wax-embedded tissue sample.

33. (currently amended) The method of claim 32 wherein said tissue sample comprises fragmented exonic RNA ~~is fragmented~~.

34. (original) The method of claim 25 wherein said biological sample is a biological fluid.

35. (original) The method of claim 25 wherein said hybridization is performed under stringent conditions.

36. (original) The method of claim 25 further comprising the step of quantifying the expression of said intronic RNA.

37. (original) The method of claim 25 wherein said polynucleotide is a single-stranded oligonucleotide.

38. (original) The method of claim 37 wherein said single-stranded oligonucleotide is a PCR probe or primer.

39. (previously presented) The method of claim 25 wherein the expression of more than one target gene is measured.

40. (previously presented) The method of claim 39 comprising simultaneous measuring of a least 50 target genes.

41. (previously presented) The method of claim 39 comprising simultaneous measuring of at least 500 target genes.

42. (previously presented) The method of claim 39 comprising simultaneous measuring of at least 10,000 target genes.

43. (previously presented) The method of any of claims 39-42 wherein intronic RNA sequences corresponding to a plurality of said target genes are displayed as an array immobilized on a solid surface.

44. (original) The method of claim 25 wherein said target gene is selected from the genes listed in Figure 6.

45–54. (canceled)

55. (currently amended) A method for amplifying intronic RNA in a fixed paraffin-embedded tissue sample representing at least one gene of interest, comprising the steps of:

(a) contacting DNA obtained by reverse transcription of RNA comprising intronic RNA, wherein the expression of the intronic RNA ~~which~~ correlates with the expression of a corresponding exonic RNA, with at least one set of PCR primers and probe corresponding to said intronic RNA; and

(b) performing PCR amplification.

56. (original) The method of claim 55 wherein said PCR primers and probe are designed based upon a unique sequence within said intronic RNA.

57. (original) The method of claim 56 wherein said sample comprises fragmented RNA representing multiple genes of interest.

58. (original) The method of claim 57 wherein said sample is contacted with a pool of PCR primers and probes designed based upon unique sequences within introns, the expression of which correlates with the expression of corresponding exons, present in said genes of interest.

59. (original) The method of claim 58 wherein said pool comprises at least one of the intron-based primer/probe sets set forth in Figure 2.

60. (original) The method of claim 58 wherein said pool comprises at least one forward or reverse primer or probe set forth in Figure 2.

61. (original) The method of claim 55 wherein said tissue sample is from a tumor biopsy.

62. (original) The method of claim 61 wherein said tumor biopsy is obtained from a human patient.

63. (previously presented) The method of claim 62 wherein said tumor is selected from the group consisting of breast cancer, lung cancer, colorectal cancer, colon cancer, prostate cancer, hepatocellular cancer, gastric cancer, pancreatic cancer, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, thyroid cancer, renal cancer, carcinoma, melanoma, and brain cancer.

64. (original) The method of claim 55 further comprising the step of determining the expression levels of the RNA transcripts of said genes of interest or their expression products.

65. (original) The method of claim 64 wherein differential expression of said RNA transcripts or their products is correlated with predicted patient response to treatment or patient survival.

66. (original) The method of claim 55 wherein said gene of interest is selected from the genes listed in Figure 6.

67. (original) The method of claim 63 wherein the tumor is invasive breast cancer, and the method comprises determining the expression levels of the RNA transcripts or expression products of a gene or gene set selected from the group consisting of:

(a) Bcl2, cyclinG1, NFKBp65, NME1, EPHX1, TOP2B, DR5, TERC, Src, DIABLO;

(b) Ki67, XIAP, hENT1, TS, CD9, p27, cyclinG1, pS2, NFKBp65, CYP3A4;

(c) GSTM1, XIAP, Ki67, TS, cyclinG1, p27, CYP3A4, pS2, NFKBp65, ErbB3;

(d) PR, NME1, XIAP, upa, cyclinG1, Contig51037, TERC, EPHX1, ALDH1A3, CTSL;

(e) CA9, NME1, TERC, cyclinG1, EPHX1, DPYD, Src, TOP2B, NFKBp65, VEGFC;

(f) TFRC, XIAP, Ki67, TS, cyclinG1, p27, CYP3A4, pS2, ErbB3, NFKBp65;

(g) Bcl2, PRAME, cyclinG1, FOXM1, NFKBp65, TS, XIAP, Ki67, CYP3A4, p27;

(h) FOXM1, cyclinG1, XIAP, Contig51037, PRAME, TS, Ki67, PDGFRa, p27, NFKBp65;

(i) PRAME, FOXM1, cyclinG1, XIAP, Contig51037, TS, Ki6, PDGFRa, p27, NFKBp65;

(j) Ki67, XIAP, PRAME, hENT1, contig51037, TS, CD9, p27, ErbB3, cyclinG1;

(k) STK15, XIAP, PRAME, PLAUR, p27, CTSL, CD18, PREP, p53, RPS6KB1;

(l) GSTM1, XIAP, PRAME, p27, Contig51037, ErbB3, GSTp, EREG, ID1, PLAUR;

(m) PR, PRAME, NME1, XIAP, PLAUR, cyclinG1, Contig51037, TERC, EPHX1, DR5;

(n) CA9, FOXM1, cyclinG1, XIAP, TS, Ki67, NFKBp65, CYP3A4, GSTM3, p27;

(o) TFRC, XIAP, PRAME, p27, Contig51037, ErbB3, DPYD, TERC, NME1, VEGFC; and

(p) CEGP1, PRAME, hENT1, XIAP, Contig51037, ErbB3, DPYD, NFKBp65, ID1, TS

in said sample;

(2) subjecting the data obtained in step (a) to statistical analysis; and

(3) determining whether the likelihood of long-term survival of said patient, without the recurrence of breast cancer has increased or decreased.

68. (original) The method of claim 67 wherein the expression levels of said RNA transcripts or their expression products are normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products.

69. (withdrawn) The method of claim 63 wherein the tumor is estrogen receptor (ER)-positive invasive breast cancer, and the method comprises

(1) determining the expression levels of the RNA transcripts or expression products of a gene or gene set selected from the group consisting of:

(a) PRAME, p27, IGFBP2, HIF1A, TIMP2, ILT2, CYP3A4, ID1, EstR1, DIABLO;

(b) Contig51037, EPHX1, Ki67, TIMP2, cyclinG1, DPYD, CYP3A4, TP, AIB1, CYP2C8;

(c) Bcl2, hENT1, FOXM1, Contig51037, cyclinG1, Contig46653, PTEN, CYP3A4, TIMP2, AREG;

(d) HIF1A, PRAME, p27, IGFBP2, TIMP2, ILT2, CYP3A4, ID1, EstR1, DIABLO;

(e) IGF1R, PRAME, EPHX1, Contig51037, cyclinG1, Bcl2, NME1, PTEN, TBP, TIMP2;

(f) FOXM1, Contig51037, VEGFC, TBP, HIF1A, DPYD, RAD51C, DCR3, cyclinG1, BAG1;

(g) EPHX1, Contig51037, Ki67, TIMP2, cyclinG1, DPYD, CYP3A4, TP, AIB1, CYP2C8;

(h) Ki67, VEGFC, VDR, GSTM3, p27, upa, ITGA7, rhoC, TERC, Pin1;

(i) CDC25B, Contig51037, hENT1, Bcl2, HLAG, TERC, NME1, upa, ID1, CYP;

(j) VEGFC, Ki67, VDR, GSTM3, p27, upa, ITGA7, rhoC, TERC, Pin1;

(k) CTSB, PRAME, p27, IGFBP2, EPHX1, CTSL, BAD, DR5, DCR3, XIAP;

(l) DIABLO, Ki67, hENT1, TIMP2, ID1, p27, KRT19, IGFBP2, TS, PDGFB;

(m) p27, PRAME, IGFBP2, HIF1A, TIMP2, ILT2, CYP3A4, ID1, EstR1, DIABLO;

(n) CDH1; PRAME, VEGFC; HIF1A; DPYD, TIMP2, CYP3A4, EstR1, RBP4, p27;

(o) IGFBP3, PRAME, p27, Bcl2, XIAP, EstR1, Ki67, TS, Src, VEGF;

(p) GSTM3, PRAME, p27, IGFBP3, XIAP, FGF2, hENT1, PTEN, EstR1, APC;

(q) hENT1, Bcl2, FOXM1, Contig51037, CyclinG1, Contig46653, PTEN, CYP3A4, TIMP2, AREG;

(r) STK15, VEGFC, PRAME, p27, GCLC, hENT1, ID1, TIMP2, EstR1, MCP1;

(s) NME1, PRAM, p27, IGFBP3, XIAP, PTEN, hENT1, Bcl2, CYP3A4, HLAG;

(t) VDR, Bcl2, p27, hENT1, p53, PI3KC2A, EIF4E, TFRC, MCM3, ID1;

(u) EIF4E, Contig51037, EPHX1, cyclinG1, Bcl2, DR5, TBP, PTEN, NME1, HER2;

(v) CCNB1, PRAME, VEGFC, HIF1A, hENT1, GCLC, TIMP2, ID1, p27, upa;

(w) ID1, PRAME, DIABLO, hENT1, p27, PDGFRa, NME1, BIN1, BRCA1, TP;

(x). FBXO5, PRAME, IGFBP3, p27, GSTM3, hENT1, XIAP, FGF2, TS, PTEN;

(y) GUS, HIA1A, VEGFC, GSTM3, DPYD, hENT1, EBXO5, CA9, CYP, KRT18; and

(z) Bclx, Bcl2, hENT1, Contig51037, HLAG, CD9, ID1, BRCA1, BIN1, HBEGF;

(2) subjecting the data obtained in step (1) to statistical analysis; and

(3) determining whether the likelihood of long-term survival of said patient, without the recurrence of breast cancer has increased or decreased.

70. (withdrawn) The method of claim 69 wherein the expression levels of said RNA transcripts or their expression products are normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products.

71. (original) The method of claim 63 wherein the tumor is breast cancer, and the method comprises

(1) determining the expression levels of the RNA transcripts or expression products of a gene or gene set selected from the group consisting of: FOXM1; PRAME; SKT15, Ki-67; CA9; NME1; SURV; TFRC; YB-1; RPS6KB1; Src; Chk1; CCNB1; Chk2; CDC25B; CYP3A4; EpCAM; VEGFC; hENT1; BRCA2; EGFR; TK1; VDR; Blc12; CEGP1; GSTM1; PR; BBC3; GATA3; DPYD; GSTM3; ID1; EstR1; p27; XIAP; IGF1R; AK055699; P13KC2A; TGFB3; BAGI1; pS2; WISP1; HNF3A; and NFKBp65, normalized against the expression levels of all RNA transcripts or their products in said sample, or of a reference set of RNA transcripts or their expression products;

(2) subjecting the data obtained in step (a) to statistical analysis; and

(3) determining whether the likelihood of long-term survival of said patient, without the recurrence of breast cancer has increased or decreased.

72. (canceled)

73. (previously presented) The method of claim 63 wherein the tumor is invasive breast cancer, and the method comprises determining the expression levels of RNA transcripts or expression products of a gene or gene set from the group consisting of:

(a) p53BP2, Bcl2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(b) GRB7, CD68, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(c) PR, p53BP2, PRAME, DIABLO, CTSL, IGFBP2, TIMP1, CA9, MMP9, and COX2;

(d) CD68, GRB7, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(e) Bcl2, p53BP2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(f) KRT14, KRT5, PRAME, p53BP2, GUS1, AIB1, MCM3, CCNE1, MCM6, and ID1;

(g) PRAME, p53BP2, EstR1, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(h) CTSL2, GRB7, TOP2A, CCNB1, Bcl2, DIABLO, PRAME, EMS1, CA9, and EpCAM;

(i) EstR1, p53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(j) Chk1, PRAME, p53BP2, GRB7, CA9, CTSL, CCNB1, TOP2A, and IGFBP2;

(k) IGFBP2, GRB7, PRAME, DIABLO, CTSL, β-Catenin, PPM1D, Chk1, WISP1, and LOT1;

(l) HER2, p53BP2, Bcl2, DIABLO, TIMP1, EPHX1, TOP2A, TRAIL, CA9, and AREG;

(m) BAG1, p53BP2, PRAME, IL6, CCNB1, PAI1, AREG, CA9, and Ki67;

(n) CEGP1, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, and AKT2, and FGF18;

(o) STK15, p53BP2, PRAME, IL6, CCNE1, AKT2, DIABLO, cMet, CCNE2, and COX2;

(p) KLK10, EstR1, p53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1,

and BBC3;

(q) AIB1, p53BP2, Bcl2, DIABLO, TIMP1, CD3, p53, CA9, GRB7, and EPHX1

(r) BBC3, GRB7, CD68, PRAME, TOP2A, CCNB1, EPHX1, CTSL GSTM1, and APC;

(s) CD9, GRB7, CD68, TOP2A, Bcl2, CCNB1, CD3, DIABLO, ID1, and PPM1D;

(t) EGFR, KRT14, GRB7, TOP2A, CCNB1, CTSL, Bcl2, TP, KLK10, and CA9;

(u) HIF1α, PR, DIABLO, PRAME, Chk1, AKT2, GRB7, CCNE1, TOP2A, and CCNB1;

(v) MDM2, p53BP2, DIABLO, Bcl2, AIB1, TIMP1, CD3, p53, CA9, and HER2;

(w) MYBL2, p53BP2, PRAME, IL6, Bcl2, DIABLO, CCNE1, EPHX1, TIMP1, and CA9;

(x) p27, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, AKT2, and ID1;

(y) RAD51, GRB7, CD68, TOP2A, CIAP2, CCNB1, BAG1, IL6, FGFR1, and p53BP2;

(z) SURV, GRB7, TOP2A, PRAME, CTSL, GSTM1, CCNB1, VDR, CA9; and CCNE2;

(aa) TOP2B, p53BP2, DIABLO, Bcl2, TIMP1, AIB1, CA9, p53, KRT8, and BAD;

(ab) ZNF217, GRB7, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, APC4, and β-Catenin,

in a breast cancer tissue sample obtained from said patient,

(2) subjecting the data obtained in step (a) to statistical analysis; and

(3) determining whether the likelihood of said long-term survival has increased or decreased.

74. (original) The method of claim 73 wherein the expression levels of said RNA transcripts or their expression products are normalized against the expression levels of all RNA transcripts or their expression products in said breast cancer tissue sample, or of a reference set of RNA transcripts or their products.

75. (currently amended) A method for measuring the expression level of at least one gene ~~expression~~ comprising measuring the level of ~~using~~ a plurality of polynucleotides capable of hybridizing to target genes of interest wherein at least one of the said polynucleotides comprises an intron-based sequence wherein the expression of said intronic sequence is confirmed to correlate ~~the expression of which correlates~~ with the expression of a corresponding exon sequence and detecting and identifying the polynucleotide-intronic complex.

76. (original) The method of claim 75 wherein all of said polynucleotides comprise intron sequences.

77. (currently amended) The method of claim 75 wherein said polynucleotides comprise ~~comprising~~ at least one of the amplicons shown in Figures 1A-M (SEQ ID NOs: 1-13), or the complement thereof.

78. (currently amended) The method of claim 75 wherein said polynucleotides comprise ~~comprising~~ two or more of the amplicons shown in Figures 1A-M (SEQ ID NOs: 1-13), or the complement thereof.

79. (currently amended) The method of claim 75 wherein said polynucleotides comprise ~~comprising~~ all of the amplicons shown in Figures 1A-M (SEQ ID NOs: 1-13), or the complement thereof.

80. (previously presented) The method of claim 75 comprising using intron-based polynucleotide sequences hybridizing to at least one gene of interest selected from the group consisting of: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-67, GSTM1, PR, BBC3, NME1, SURV, GATA3, TFRC, YB-1, DPYD, CA9, Contig51037, RPS6K1 and Her2, wherein at least 80% of the sequences are intron-based.

81. (original) The method of claim 80 comprising using intron-based polynucleotide sequences hybridizing to at least 5 of said genes.

82. (original) The method of claim 80 comprising using intron-based polynucleotide sequences hybridizing to at least 10 of said genes.

83. (original) The method of claim 80 comprising using intron-based polynucleotide sequences hybridizing to all of said genes.

84. (original) The method of claim 75 comprising using intron-based polynucleotide sequences hybridizing to at least one gene of interest selected from the group consisting of: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-67, GSTM1, CA9, PR, BBC3, NME1, SURV, GATA3, TFRC, YB-1, DPYD, GSTM3, RPS6KB1, Src, Chk1, ID1, EstR1, p27, CCNB1, XIAP, Chk2, CDC25B, IGF1R, AK055699, P13KC2A, TGFB3, BAGI1, CYP3A4, EpCAM, VEGFC, pS2, hENT1, WISP1, HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IF1A, CDH1, HIF1α, IGFBP3, CTSB, Her2 and DIABLO.

85. (original) The method of claim 84 comprising using intron-based polynucleotide sequences hybridizing to at least 5 of said genes.

86. (original) The method of claim 84 comprising using intron-based polynucleotide sequences hybridizing to at least 10 of said genes.

87. (previously presented) The method of claim 84 comprising using intron-based polynucleotide sequences hybridizing to all of said genes.

88. (original) The method of claim 75 comprising using intron-based polynucleotide sequences hybridizing to at least one gene set selected from the group consisting of:

(a) Bcl2, cyclinG1, NFKBp65, NME1, EPHX1, TOP2B, DR5, TERC, Src, DIABLO;

(b) Ki67, XIAP, hENT1, TS, CD9, p27, cyclinG1, pS2, NFKBp65, CYP3A4;

(c) GSTM1, XIAP, Ki67, TS, cyclinG1, p27, CYP3A4, pS2, NFKBp65, ErbB3;

(d) PR, NME1, XIAP, upa, cyclinG1, Contig51037, TERC, EPHX1, ALDH1A3, CTSL;

(e) CA9, NME1, TERC, cyclinG1, EPHX1, DPYD, Src, TOP2B, NFKBp65, VEGFC;

(f) TFRC, XIAP, Ki67, TS, cyclinG1, p27, CYP3A4, pS2, ErbB3, NFKBp65;

(g) Bcl2, PRAME, cyclinG1, FOXM1, NFKBp65, TS, XIAP, Ki67, CYP3A4, p27;

(h) FOXM1, cyclinG1, XIAP, Contig51037, PRAME, TS, Ki67, PDGFRa, p27,

NFKBp65;

(i) PRAME, FOXM1, cyclinG1, XIAP, Contig51037, TS, Ki6, PDGFRa, p27, NFKBp65;

(j) Ki67, XIAP, PRAME, hENT1, contig51037, TS, CD9, p27, ErbB3, cyclinG1;

(k) STK15, XIAP, PRAME, PLAUR, p27, CTSL, CD18, PREP, p53, RPS6KB1;

(l) GSTM1, XIAP, PRAME, p27, Contig51037, ErbB3, GSTp, EREG, ID1, PLAUR;

(m) PR, PRAME, NME1, XIAP, PLAUR, cyclinG1, Contig51037, TERC, EPHX1, DR5;

(n) CA9, FOXM1, cyclinG1, XIAP, TS, Ki67, NFKBp65, CYP3A4, GSTM3, p27;

(o) TFRC, XIAP, PRAME, p27, Contig51037, ErbB3, DPYD, TERC, NME1, VEGFC; and

(p) CEGP1, PRAME, hENT1, XIAP, Contig51037, ErbB3, DPYD, NFKBp65, ID1, TS.

89. (withdrawn) The method of claim 75 comprising using intron-based polynucleotide sequences hybridizing to at least one gene set selected from the group consisting of:

(a) PRAME, p27, IGFBP2, HIF1A, TIMP2, ILT2, CYP3A4, ID1, EstR1, DIABLO;

(b) Contig51037, EPHX1, Ki67, TIMP2, cyclinG1, DPYD, CYP3A4, TP, AIB1, CYP2C8;

(c) Bcl2, hENT1, FOXM1, Contig51037, cyclinG1, Contig46653, PTEN, CYP3A4, TIMP2, AREG;

(d) HIF1A, PRAME, p27, IGFBP2, TIMP2, ILT2, CYP3A4, ID1, EstR1, DIABLO;

(e) IGF1R, PRAME, EPHX1, Contig51037, cyclinG1, Bcl2, NME1, PTEN, TBP, TIMP2;

(f) FOXM1, Contig51037, VEGFC, TBP, HIF1A, DPYD, RAD51C, DCR3, cyclinG1, BAG1;

(g) EPHX1, Contig51037, Ki67, TIMP2, cyclinG1, DPYD, CYP3A4, TP, AIB1, CYP2C8;

(h) Ki67, VEGFC, VDR, GSTM3, p27, upa, ITGA7, rhoC, TERC, Pin1;

(i) CDC25B, Contig51037, hENT1, Bcl2, HLAG, TERC, NME1, upa, ID1, CYP;

(j) VEGFC, Ki67, VDR, GSTM3, p27, upa, ITGA7, rhoC, TERC, Pin1;

(k) CTSB, PRAME, p27, IGFBP2, EPHX1, CTSL, BAD, DR5, DCR3, XIAP;

(l) DIABLO, Ki67, hENT1, TIMP2, ID1, p27, KRT19, IGFBP2, TS, PDGFB;

(m) p27, PRAME, IGFBP2, HIF1A, TIMP2, ILT2, CYP3A4, ID1, EstR1, DIABLO;

(n) CDH1; PRAME, VEGFC; HIF1A; DPYD, TIMP2, CYP3A4, EstR1, RBP4, p27;

(o) IGFBP3, PRAME, p27, Bcl2, XIAP, EstR1, Ki67, TS, Src, VEGF;

(p) GSTM3, PRAME, p27, IGFBP3, XIAP, FGF2, hENT1, PTEN, EstR1, APC;

(q) hENT1, Bcl2, FOXM1, Contig51037, CyclinG1, Contig46653, PTEN, CYP3A4, TIMP2, AREG;

(r) STK15, VEGFC, PRAME, p27, GCLC, hENT1, ID1, TIMP2, EstR1, MCP1;

(s) NME1, PRAM, p27, IGFBP3, XIAP, PTEN, hENT1, Bcl2, CYP3A4, HLAG;

(t) VDR, Bcl2, p27, hENT1, p53, PI3KC2A, EIF4E, TFRC, MCM3, ID1;

(u) EIF4E, Contig51037, EPHX1, cyclinG1, Bcl2, DR5, TBP, PTEN, NME1, HER2;

(v) CCNB1, PRAME, VEGFC, HIF1A, hENT1, GCLC, TIMP2, ID1, p27, upa;

(w) ID1, PRAME, DIABLO, hENT1, p27, PDGFRa, NME1, BIN1, BRCA1, TP;

(x) FBXO5, PRAME, IGFBP3, p27, GSTM3, hENT1, XIAP, FGF2, TS, PTEN;

(y) GUS, HIA1A, VEGFC, GSTM3, DPYD, hENT1, EBXO5, CA9, CYP, KRT18; and

(z) Bclx, Bcl2, hENT1, Contig51037, HLAG, CD9, ID1, BRCA1, BIN1, HBEGF.

90. (previously presented) The method of claim 75 comprising using intron-based polynucleotide sequences hybridizing to at least one gene set selected from the group consisting of:

(a) p53BP2, Bcl2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(b) GRB7, CD68, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(c) PR, p53BP2, PRAME, DIABLO, CTSL, IGFBP2, TIMP1, CA9, MMP9, and COX2;

(d) CD68, GRB7, TOP2A, Bcl2, DIABLO, CD3, ID1, PPM1D, MCM6, and WISP1;

(e) Bcl2, p53BP2, BAD, EPHX1, PDGFRβ, DIABLO, XIAP, YB1, CA9, and KRT8;

(f) KRT14, KRT5, PRAME, p53BP2, GUS1, AIB1, MCM3, CCNE1, MCM6, and ID1;

(g) PRAME, p53BP2, EstR1, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(h) CTSL2, GRB7, TOP2A, CCNB1, Bcl2, DIABLO, PRAME, EMS1, CA9, and EpCAM;

(i) EstR1, p53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, BBC3, and VEGFB;

(j) Chk1, PRAME, p53BP2, GRB7, CA9, CTSL, CCNB1, TOP2A, and IGFBP2;

(k) IGFBP2, GRB7, PRAME, DIABLO, CTSL, β-Catenin, PPM1D, Chk1, WISP1, and LOT1;

(l) HER2, p53BP2, Bcl2, DIABLO, TIMP1, EPHX1, TOP2A, TRAIL, CA9, and AREG;

(m) BAG1, p53BP2, PRAME, IL6, CCNB1, PAI1, AREG, CA9, and Ki67;

(n) CEGP1, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, and AKT2, and FGF18;

(o) STK15, p53BP2, PRAME, IL6, CCNE1, AKT2, DIABLO, cMet, CCNE2, and COX2;

(p) KLK10, EstR1, p53BP2, PRAME, DIABLO, CTSL, PPM1D, GRB7, DAPK1, and BBC3;

(q) AIB1, p53BP2, Bcl2, DIABLO, TIMP1, CD3, p53, CA9, GRB7, and EPHX1

(r) BBC3, GRB7, CD68, PRAME, TOP2A, CCNB1, EPHX1, CTSL GSTM1, and APC;

(s) CD9, GRB7, CD68, TOP2A, Bcl2, CCNB1, CD3, DIABLO, ID1, and PPM1D;

(t) EGFR, KRT14, GRB7, TOP2A, CCNB1, CTSL, Bcl2, TP, KLK10, and CA9;

(u) HIF1α, PR, DIABLO, PRAME, Chk1, AKT2, GRB7, CCNE1, TOP2A, and CCNB1;

(v) MDM2, p53BP2, DIABLO, Bcl2, AIB1, TIMP1, CD3, p53, CA9, and HER2;

(w) MYBL2, p53BP2, PRAME, IL6, Bcl2, DIABLO, CCNE1, EPHX1, TIMP1, and CA9;

(x) p27, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, STK15, AKT2, and ID1;

(y) RAD51, GRB7, CD68, TOP2A, CIAP2, CCNB1, BAG1, IL6, FGFR1, and p53BP2;

(z) SURV, GRB7, TOP2A, PRAME, CTSL, GSTM1, CCNB1, VDR, CA9; and CCNE2;

(aa) TOP2B, p53BP2, DIABLO, Bcl2, TIMP1, AIB1, CA9, p53, KRT8, and BAD; and

(ab) ZNF217, GRB7, p53BP2, PRAME, DIABLO, Bcl2, COX2, CCNE1, APC4, and β-Catenin.

91. (previously presented) The method of claim 75 comprising intron-based polynucleotide sequences hybridizing to at least one genes selected from the group consisting of: IGFR1; BCl2; HNF3A; TP53BP2; GATA3; BBC3; RAD51C; BAG1; IGFBP2; PR; CD9; RB1; EPHX1; CEGP1; TRAIL; DR5; p27; p53; MTA; RIZ1; ErbB3; TOP2B; EIF4E, CD68; CTSL; FBXO5; SURV; CCNB1; MCM2; Chk1; MYBL2; HIF1A; cMET; EGFR; TS; and STK15.

92. (original) The method of claim 75 comprising intron-based polynucleotide sequences hybridizing to at least one genes selected from the group consisting of B-actin; BAG1; bcl-2; CCNB1; CD68; CEGP1; CTSL2; EstR1; GAPDH; GSTM1; GUS; GRB7; HER2; Ki-67; MYBL2; PR; RPLPO; STK15; STMY3; SURVIVIN; and TFRC.

93. (original) The method of claim 75 comprising using intron-based polynucleotide sequences corresponding to at least one gene selected from the genes listed in Figure 6.

94. (original) The method of claim 75 comprising using intron-based polynucleotide sequences corresponding to a plurality of genes selected from the genes listed in Figure 6.

95. (original) The method of claim 75 comprising using both intron-based and exon-based polynucleotide sequences.

96. (original) The method of claim 95 comprising using both intron-based and exon-based polynucleotide sequences hybridizing to the same target gene of interest.

97. (previously presented) The method of claim 100 wherein said array comprises at least 100 genes.

98. (currently amended) The method of claim 100 wherein said array comprises at least 100 genes in a 100 μm^2 ~~μ~~ section.

99. (currently amended) The method of claim 100 wherein said array comprises at least 150 genes in a 100 μm^2 ~~μ~~ section.

100. (currently amended) The method of claim 75 wherein the plurality of polynucleotides ~~polypeptides~~ is immobilized on a solid surface in an array.

101. (previously presented) The method of claim 25 comprising using both intron-based and exon-based polynucleotide sequences.

102 (previously presented) The method of claim 55 comprising using both intron-based and exon-based polynucleotide sequences.

103. (new) A method for classifying a tumor sample according to the likelihood of cancer recurrence or response to therapy in a mammalian subject, comprising

(a) measuring gene expression in the tumor sample, comprising

(i) providing a polynucleotide complementary to an intronic RNA sequence within a target gene, wherein the expression of said intronic RNA sequence has been confirmed to correlate with the expression of an exonic mRNA sequence within said genes;

(ii) hybridizing said polynucleotide to said intronic RNA sequence to form a polynucleotide-intronic RNA complex; and

(iii) detecting and identifying the polynucleotide-intronic RNA complex; and

(iv) determining the gene expression level of the gene in the tumor sample;

(b) making a prognostic decision regarding cancer recurrence or response to therapy.